

APPLICANTS: Fouser et al.
U.S.S.N.: 10/047,264

For the alignment shown, gap weight = 8, average match = 2.912, length weight = 2, average mismatch = -2.003, quality = 829, length = 1101, ratio = 3.589, gaps = 1. The two proteins were found to be 69.565% similar and 66.957% identical.

B2
Pursuant to 37 CFR 1.121(b)(1)(iii), a marked up version of the specification showing the changes made appears as Appendix A of this Amendment.

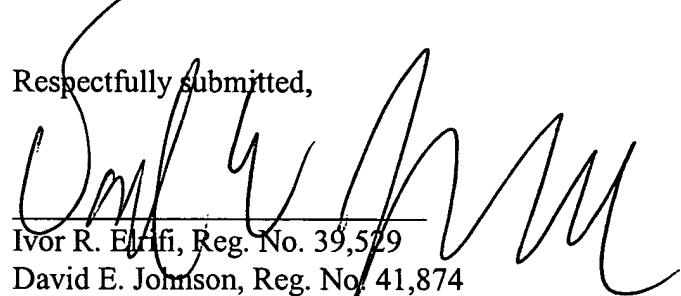
REMARKS

Applicants have amended the text to insert the appropriate SEQ ID NOs corresponding to the sequence listing submitted with the Notice to Comply with Sequence Listing Requirement, mailed February 13, 2002. No new matter is added.

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The Commissioner is hereby authorized to charge any additional fees that may be due, or credit any overpayment of same, to Deposit Account No. 50-0311, Attorney Reference No. 22058-532. Should any questions or issues arise concerning this application, the Examiner is encouraged to contact the undersigned at the telephone number provided below.

Respectfully submitted,


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Dated: June 18, 2002

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Appendix A: marked up version of the specification showing the changes made

In the Specification:

Mark-up of changes to the text at page 12, line 1 through line 4:

(amended once) An alignment between the Q9YGC8 gallus gallus (chicken) interleukin-10 receptor 2 (5/1999) (SEQ ID NO:8) and amino acids 30-227 of the amino acid sequence (SEQ ID NO:33) shown in Table 2 is provided below. For the alignment shown, length = 341, Score = 73.4, bits (177.0), Expect = $1e^{-12}$, identities = 56/200 (28%), and positives = 92/200, (46%).

Mark-up of changes to the text at page 75, line 7 through line 12:

The amino acid sequences of human CRF2-12 (SEQ ID NO:34) and murine CRF2-12 (SEQ ID NO:35) polypeptides were compared. The alignment is presented below. Alignments were prepared as described in Henikoff et al., Proc. Natl. Acad. Sci. (USA) 89:10915-19, 1992. For the alignment shown, gap weight = 8, average match = 2.912, length weight = 2, average mismatch = -2.003, quality = 829, length = 1101, ratio = 3.589, gaps = 1. The two proteins were found to be 69.565% similar and 66.957% identical.

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